## SEQUENCE LISTING

<110> PARANHOS-BACCALA, Glaucia

LESENECHAL, Mylene

JOLIVET, Michel



26

<120> TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS OF DETECTING AND TREATING CHAGAS DISEASE

<130> WPB 36400B

<140> US 09/138,735

<141> 1998-08-24

<150> US 08/480,917

<151> 1995-06-07

<150> FR 94/10132

<151> 1994-08-12

<160> 13

<170> PatentIn version 3.0

<210> 1

<211> 3402

<212> DNA

<400> 1

<213> Trypanosoma cruzi

Cove

60 aacgctatta ttagaacagt ttctgtacta tattgtcatt tggggagggg ggaaaggggg 120 gaagtacttg ccgttttgtg tgggtgacga gacaacacac atcgagcggg aagaaaaaa aaaaggaaat aaattaaatt aaattatttg ttctttgaat aggcaaagaa gaagaagaag 180 240 300 ggaaataaca acgcaaggcg cggacatgac cgtgacggtg gatttgttca atcatgcgaa gccgagcaac aatgagggcc gcgtgtggtc tgtggacgcc gcgacattta acgaggtgcc 360 tgaggcgcag cgtgtgctgg cggattcgca gttttatctt gcctacacca tgaagcggcg 420 tcacgtgctg cgtgtggtga agcgctcgaa ccttttgaag ggcaccgtgc gggcacactc 480 540 aaagcccatt catgcggtga agtttgtgaa ttaccgcagt aacgtcgcag catcggctgg

gaagggggag ttcttcgtgt gggttgtgac ggatgaaacg gaggcgagca acggcaagcc 600 ggatctcgca gcccgcctca cagtgaaggt gtactttaag cttcaggatc ctgtcacaat 660 tccatgcttt tctttcttta tcaacgccga gagtcagcgg cctgatctgc ttgtccttta 720 cgaaacgcag gcggcaattc ttgacagctc ctccctcatt gagcgctttg acgtggaatc 780 actggaggca acactacagc ggaattgcac aaccctgcga accctgactc aaccggttag 840 tgagaacagt ttatgctccg ttggctctgg cggatggttc acctttacca cggaaccaac 900 aatggtagcg gcatgcacat tacgaaaccg cagcactcca tcatgggcgt gttgcgaggg 960 tgagccagtg aaggcattgc atctccttga cgcaaccgtt gaggaaaatg tcagtgttct 1020 cgtggccgca tctacaaaag gggtgtacca atggctcctt acgggtgtag cagaaccaaa 1080 cttgttgcgc aagtttgtca ttgatggatc tattgtcgcg atggaaagct cacgagaaac 1140 gtttgccgtg tttgacgaca ggaagcagct ggcgctggtc aacatgcatt cccctcataa 1200 ctttacctgc acacactaca tgatgccttg tcaggtacag cgtaacggct tttgcttcaa 1260 tcgtacagcc gacggtagct gcgtcctggc tgacatgtcg attcgattga cgatcttcca 1320 1380 tctccggtcc tcccgcaggg aagaacagca gccaggccaa aaaacatcgg tagtggcgac 1440 ggcgaaaccg gggtgtgtgt cctcgggcac tgacgcggcg agtagcagtc ataccaatac

De

gacttctgcc gctgctgcat cccctgcatc accccctgtt tcagcgccag ccaaggcagc 1500 cgcgcctcct gccgcggcgc gatcggctga gccgcacgtg gggagcaaga tcattgctaa 1560 tctagtgaat cagctgggga ttaatgtcac ccaaaggagc gtcgtcagca ctggagcgcc 1620 ggccacgacg aggtctacgg cggtgacgtc cacgactacc gccccgcagc gaacaagtcc 1680 atacgggcac aatggccgac ctgtgacggc tggattggtg gcagctaata gtggtgccag 1740 cgcggcctcg tctcccacag ccgcggcgaa accaacagga gaagaaaagg cctccgcggc 1800 1860 atgtgaaacg agctccgtgg cgataaatgc gacacgcccg gcgcttcaca acgcctctct cccgcaggcg ccaacggatg gcgttttggc ggcagcagta taccagtcgg agggcgaggt 1920 1980 tcatcagtcg ctggagcggc tggagtccgt cataaccaac acgtctcggg ttctgaagtt 2040 gctccctgac accattcgaa gagaccatga acaacttctg aatctgggtt tagaggcaca 2100 gatgacagag ctgcagcaga gccgtccaac accgcaaaca cagccgagag acacaagctc cgcgaaatca tccgtgtttg agacgtacac ccttgttctc attgcggatt ccctctctcg 2160 2220 caacatcacg aagggggtga agcgtggtgt gaacgaggcc attatgttgc atctcgacca 2280 tgaggtgcgg cacgccatag ggaaccggct tcggcaaaca caaaagaaca tcatcaagag ccgcctcgat gaagcgttga aggaaagcac tacacagttt acggctcaat tgacgcaaac 2340 2400 ggtggagaat ctggtgaagc gcgagcttgc cgaggtgctt ggtagcatca acggctccct

26 Cons

cacttetete gtgaaggaaa atgeeteatt acagaaagag ttgaatteea taatgtetag 2460 tggggtgttg gatgaaatgc gtcgtatgcg ggaagagctg tgcacattgc gagagtccgt 2520 tgcgaagcgg aaggcaacaa tgccagattc ttctcttcac gccacgagct cctttcaagg 2580 aagaaggtet gegeeegaga caattettge aacegegtta tegatggtge gagageagea 2640 ataccgtcag ggactggaat acatgttgat ggctcagcag ccctctctcc tcctgcggtt 2700 cctcagcata cttacaaggg aaaacgaaaa cgcctactcg gaacttattg aaaatgtaga 2760 2820 gacgccgaat gacgtgtggt gttcggttct gttgcaactc atagaggccg cggcgaccga 2880 ggctgagaag gaggtggttg ttggcgtcgc cattgatatt ctctccgagc gcgatcaaat 2940 tgctcagaac ggcgcactcg gctcgaaact caccaccgcc atgcgagcct ttgagcgaca 3000 ggcaaggtcg gagacaacga gcaggtcatt cttgcaatgc ctgaagaacc tggaaaagct 3060 tctgcaatca tgataataaa aagaactcaa cgaatacagt tgttgattat taaggaaggg 3120 aaaagagaga aagagagaga gagagagaga aatgtaatgg gcgtttagtt acggtagaaa gaaaacgtgt ggataagaag gaggggtttt gtgtgcgacc aggaattact ggggaacgct 3180 gctacacggc ggaatcgacc attitattat tattattatt gtctttagta ttatgttttt 3240 tcttgtgtgt gtgtgtgt gtttgtgtgt gtgcggttat tttgtatccg tttgctcccg 3300

NG

cccctgccc ccatcacccg aggagaaagt agaataagac acatacgatt gttgtttttg 3360

3402

<210> 2

<211> 915

<212> PRT

<213> Trypanosoma cruzi

<400> 2

Met Thr Val Thr Val Asp Leu Phe Asn His Ala Lys Pro Ser Asn Asn

1 5 10 15

Glu Gly Arg Val Trp Ser Val Asp Ala Ala Thr Phe Asn Glu Val Pro
20 25 30

Glu Ala Gln Arg Val Leu Ala Asp Ser Gln Phe Tyr Leu Ala Tyr Thr
35 40 45

Met Lys Arg Arg His Val Leu Arg Val Val Lys Arg Ser Asn Leu Leu 50 55 60

Lys Gly Thr Val Arg Ala His Ser Lys Pro Ile His Ala Val Lys Phe
65 70 75 80

Val	Asn	Tyr	Arg	Ser	Asn	Val	Ala	Ala	Ser	Ala	Gly	Lys	Gly	Glu	Phe
				85					90					95	

Phe Val Trp Val Val Thr Asp Glu Thr Asp Ala Ser Asn Gly Lys Pro

100 105 110

Asp Leu Ala Ala Arg Leu Thr Val Lys Val Tyr Phe Lys Leu Gln Asp

Pro Val Thr Ile Pro Cys Phe Ser Phe Phe Ile Asn Ala Glu Ser Gln
130 135 140

Arg Pro Asp Leu Leu Val Leu Tyr Glu Thr Gln Ala Ala Ile Leu Asp 145 150 155 160

Ser Ser Ser Leu Ile Glu Arg Phe Asp Val Glu Ser Leu Glu Ala Thr
165 170 175

Leu Gln Arg Asn Cys Thr Thr Leu Arg Thr Leu Thr Gln Pro Val Ser
180 185 190

Glu Asn Ser Leu Cys Ser Val Gly Ser Gly Gly Trp Phe Thr Phe Thr

195 200 205

Thr Glu Pro Thr Met Val Ala Ala Cys Thr Leu Arg Asn Arg Ser Thr
210 215 220

Pro Ser Trp Ala Cys Cys Glu Gly Glu Pro Val Lys Ala Leu His Leu 225 230 235 240

Leu Asp Ala Thr Val Glu Glu Asn Val Ser Val Leu Val Ala Ala Ser

				245					250					255	
Thr	Lys	Gly	Val 260	Tyr	Gln	Trp	Leu	Leu 265	Thr	Gly	Val	Ala	Glu 270	Pro	Ası
Leu	Leu	Arg 275	Lys	Phe	Val	Ile	Asp 280	Gly	Ser	Ile	Val	Ala 285	Met	Glu	Se
Ser	Arg 290	Glu	Thr	Phe	Ala	Val 295	Phe	Asp	Asp	Arg	Lys 300	Gln	Leu	Ala	Let
Val	Asn	Met	His	Ser	Pro 310	His	Asn	Phe	Thr	Cys 315	Thr	His	Tyr	Met	Met
Pro	Cys	Gln	Val	Gln 325	Arg	Asn	Gly	Phe	Cys 330	Phe	Asn	Arg	Thr	Ala 335	Ası
Gly	Ser	Cys	Val	Leu	Ala	Asp	Met	Ser 345	Asn	Arg	Leu	Thr	Ile 350	Phe	His
Leu	Arg	Cys	Ser	Arg	Arg	Glu	Glu 360		Gln	Pro	Gly	Gln 365	Lys	Thr	Se:
Val	Val 370	Ala	Thr	Ala	Lys	Pro 375	Gly	Cys	Val	Ser	Ser	Gly	Thr	Asp	Ala
Ala 385		Ser	Ser	His	Thr		Thr	Thr	Ser	Ala	Ala	Ala	Ala	Ser	Pr:

Ala	Ser	Pro	Pro	Val	Ser	Ala	Pro	Ala	Lys	Ala	Ala	Ala	Pro	Pro	Ala
				405					410					415	

Ala Ala Arg Ser Ala Glu Pro His Val Gly Ser Lys Ile Ile Ala Asn
420 425 430

Leu Val Asn Gln Leu Gly Ile Asn Val Thr Gln Arg Ser Val Val Ser
435 440 445

Thr Gly Ala Pro Ala Thr Thr Arg Ser Thr Ala Val Thr Ser Thr Thr
450 455 460

Thr Ala Pro Gln Arg Thr Ser Pro Tyr Gly His Asn Gly Arg Pro Val
465 470 475 480

Thr Ala Gly Leu Val Ala Ala Asn Ser Gly Ala Ser Ala Ala Ser Ser
485 490 495

Pro Thr Ala Ala Lys Pro Thr Gly Glu Glu Lys Ala Ser Ala Ala
500 505 510

Cys Glu Thr Ser Ser Val Ala Ile Asn Ala Thr Arg Pro Ala Leu His
515 520 525

Asn Ala Ser Leu Pro Gln Ala Pro Thr Asp Gly Val Leu Ala Ala Ala 530 540

Val Tyr Gln Ser Glu Gly Glu Val His Gln Ser Leu Glu Arg Leu Glu
545 550 555 560

Ser	Val	Ile	Thr	Asn	Thr	Ser	Arg	Val	Leu	Lys	Leu	Leu	Pro	Asp	Thr
				565					570					575	

Ile Arg Arg Asp His Glu Gln Leu Leu Asn Leu Gly Leu Glu Ala Gln
580 585 590

Met Thr Glu Leu Gln Gln Ser Arg Pro Thr Pro Gln Thr Gln Pro Arg
595 600 605

Asp Thr Ser Ser Ala Lys Ser Ser Val Phe Glu Thr Tyr Thr Leu Val 610 620

Leu Ile Ala Asp Ser Leu Ser Arg Asn Ile Thr Lys Gly Val Lys Arg 625 630 635 640

Gly Val Asn Glu Ala Ile Met Leu His Leu Asp His Glu Val Arg His
645 650 655

Ala Ile Gly Asn Arg Leu Arg Gln Thr Gln Lys Asn Ile Ile Lys Ser
660 665 670

Arg Leu Asp Glu Ala Leu Lys Glu Ser Thr Thr Gln Phe Thr Ala Gln
675 680 685

Leu Thr Gln Thr Val Glu Asn Leu Val Lys Arg Glu Leu Ala Glu Val
690 695 700

Leu Gly Ser Ile Asn Gly Ser Leu Thr Ser Leu Val Lys Glu Asn Ala
705 710 715 720

Ser	Leu	Lys	Lys	Glu	Leu	Asn	Ser	Ile	Met	Ser	Ser	Gly	Val	Leu	Asp
				725					730					735	

Glu Met Arg Arg Met Arg Glu Glu Leu Cys Thr Leu Arg Glu Ser Val
740 745 750

Ala Lys Arg Lys Ala Thr Met Pro Asp Ser Ser Leu His Ala Thr Ser
755 760 765

Ser Phe Gln Gly Arg Arg Ser Ala Pro Glu Thr Ile Leu Ala Thr Ala 770 775 780

Leu Ser Met Val Arg Glu Gln Gln Tyr Arg Gln Gly Leu Glu Val Met
785 790 795 800

Leu Met Ala Gln Gln Pro Ser Leu Leu Leu Arg Phe Leu Ser Ile Leu 805 810 815

Thr Arg Glu Asn Glu Asn Ala Tyr Ser Glu Leu Ile Glu Asn Val Glu
820 825 830

Thr Pro Asn Asp Val Trp Cys Ser Val Leu Leu Gln Leu Ile Glu Ala 835 840 845

Ala Ala Thr Glu Ala Glu Lys Glu Val Val Val Gly Val Ala Ile Asp
850 855 860

IleLeuSerGluArgAspGlnIleAlaGlnAsnGlyAlaLeuGlySer865870875880

Lys Leu Thr Thr Ala Met Arg Ala Phe Glu Arg Gln Ala Arg Ser Glu
885 890 895

Thr Thr Ser Arg Ser Phe Leu Gln Cys Leu Lys Asn Leu Ile Lys Leu
900 . 905 910

Leu Gln Ser

915

<210> 3

<211> 24

<212> DNA

<213> Artificial

<220>

<223> phage DNA primer

<400> 3

ggtggcgacg actcctggag cccg

<210> 4

<211> 24

<212> DNA

<213> Artificial

24

<220>			
<223>	phage DNA primer	•	
<400>	Δ		
	ccag accaactggt aatg		24
009			
		·	
<210>	5		
<211>	18		
<212>	DNA		
<213>	Artificial		•
<220>			
(220)			
<223>	primer		
<400>	5		
	actg acgcggcg		18
<210>	6		
<211>	24		
<212>	DNA	·	
<213>	Artificial		

Č

<220>		
<223>	phage lambda gt10 DNA primer	
<400>	6	
cttatg	agta tttcttccag ggta	24
<210>	7	
<211>	21	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	probe/primer	
<400>	7	
	atta ttàgaacagt t	21
	·	

<210> 8 <211> 18

<212> DNA

<213> Artificial

<220>		
<223>	probe/primer	
<400>	8	
tgcagc	agcg gcagaagt	18
<210>	9	
<211>	22	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	probe/primer	
<400>	9	
cagccg	acgg tagctgcgtc ct	22
<210>	10	
<211>	21	
<212>	DNA	
<213>	Artificial	

<220>

<223>	probe/primer	
<400>	10	
acataa	tggc ctcgttcaca c	21
<210>	11	
<211>	34	
<212>	DNA	
<213>	Artificial	
		-
<220>		
<223>	probe/primer	
4400>		
	11 ctgc agatcgattt tttttttt tttt	34
<210>	12	
<211>	21	
<212>	DNA	
<213>	Artificial	
<220>		

<223> probe/primer

<400> 12

cgaagagacc atgaacaact t

21

. <210> 13

<211> 18

26

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 13

gactcgctgc agatcgat

18